Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 18:26:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524441.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10524441 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524441.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 18:26:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524441.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,741,736
Mapped reads	2,533,595 / 92.41%
Unmapped reads	208,141 / 7.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,659 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	154,577 / 5.64%
Duplication rate	4.64%
Clipped reads	2,532,293 / 92.36%

2.2. ACGT Content

Number/percentage of A's	36,827,563 / 24.92%
Number/percentage of C's	27,291,766 / 18.47%
Number/percentage of T's	47,569,683 / 32.19%
Number/percentage of G's	36,076,079 / 24.41%
Number/percentage of N's	2,866 / 0%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.4038

2.4. Mapping Quality

Mean Mapping Quality	46.02

2.5. Mismatches and indels

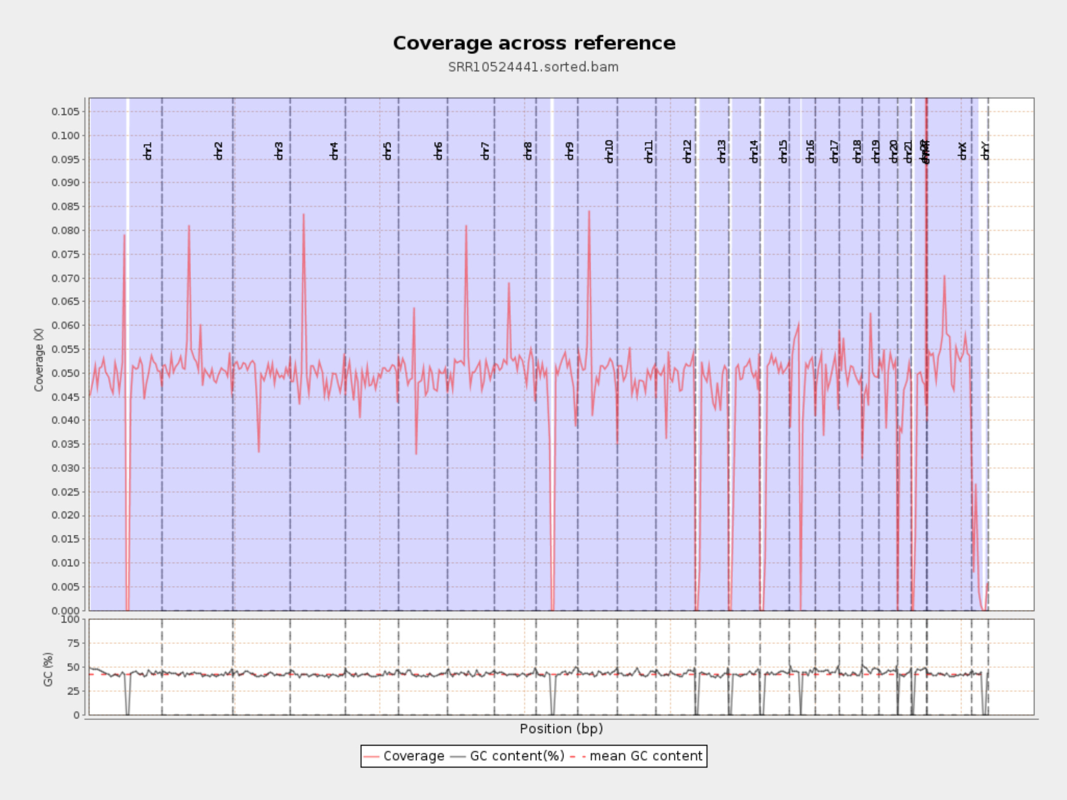
General error rate	0.48%
Mismatches	680,448
Insertions	11,076
Mapped reads with at least one insertion	0.43%
Deletions	27,264
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.46%

2.6. Chromosome stats

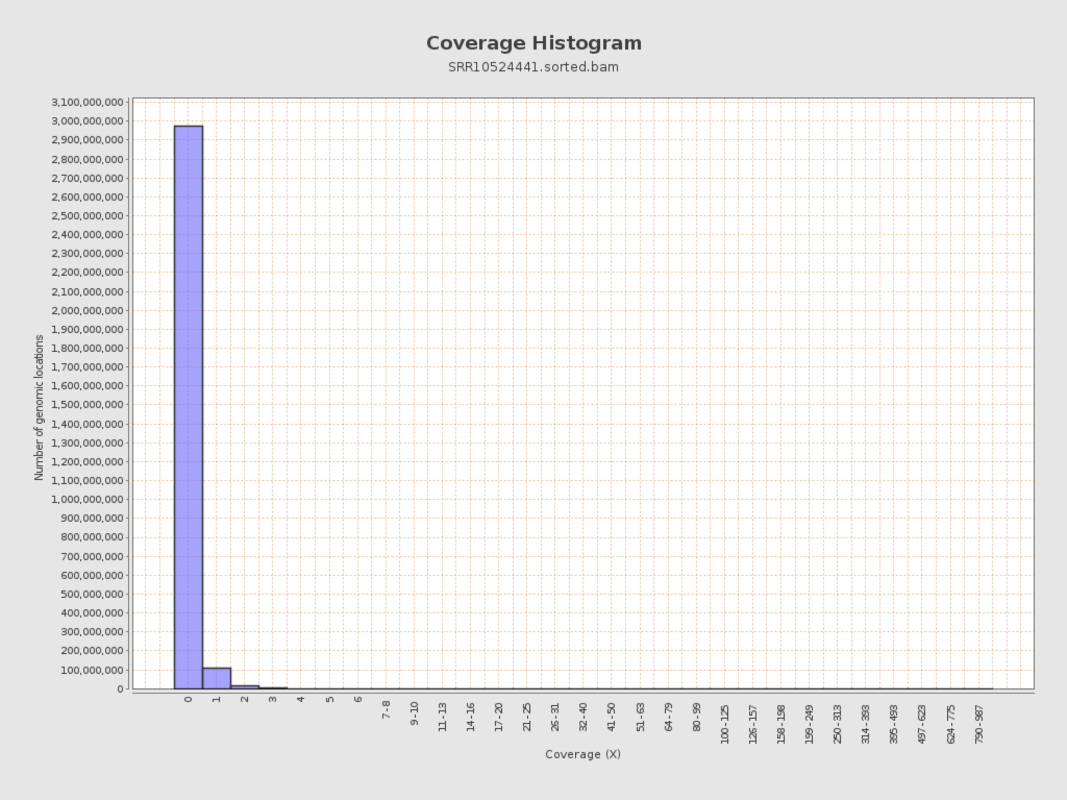
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11858251	0.0476	0.7511
chr2	243199373	12706819	0.0522	0.4682
chr3	198022430	9842255	0.0497	0.2593
chr4	191154276	9595156	0.0502	0.3101
chr5	180915260	8847909	0.0489	0.2595
chr6	171115067	8422327	0.0492	0.3299
chr7	159138663	8268692	0.052	0.5733

chr8	146364022	7692766	0.0526	0.3883
chr9	141213431	6190196	0.0438	0.3462
chr10	135534747	7076860	0.0522	0.3916
chr11	135006516	6627013	0.0491	0.3901
chr12	133851895	6616891	0.0494	0.2634
chr13	115169878	4611282	0.04	0.2378
chr14	107349540	4472389	0.0417	0.2426
chr15	102531392	4235332	0.0413	0.2534
chr16	90354753	4277540	0.0473	0.2779
chr17	81195210	3939760	0.0485	0.2783
chr18	78077248	3972127	0.0509	0.6193
chr19	59128983	2883617	0.0488	0.5232
chr20	63025520	3150084	0.05	0.2673
chr21	48129895	1963155	0.0408	0.2597
chr22	51304566	1720201	0.0335	0.2132
chrMT	16571	15318	0.9244	1.2077
chrX	155270560	8378250	0.054	0.3123
chrY	59373566	450132	0.0076	0.1901

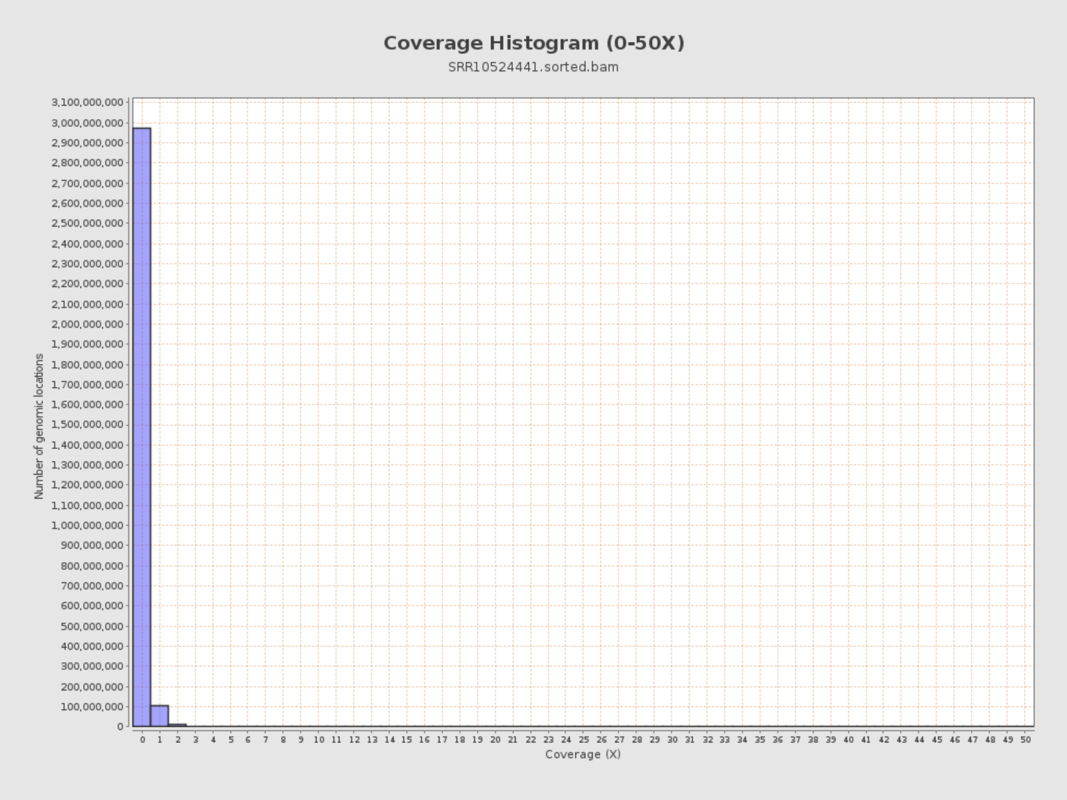
3. Results : Coverage across reference



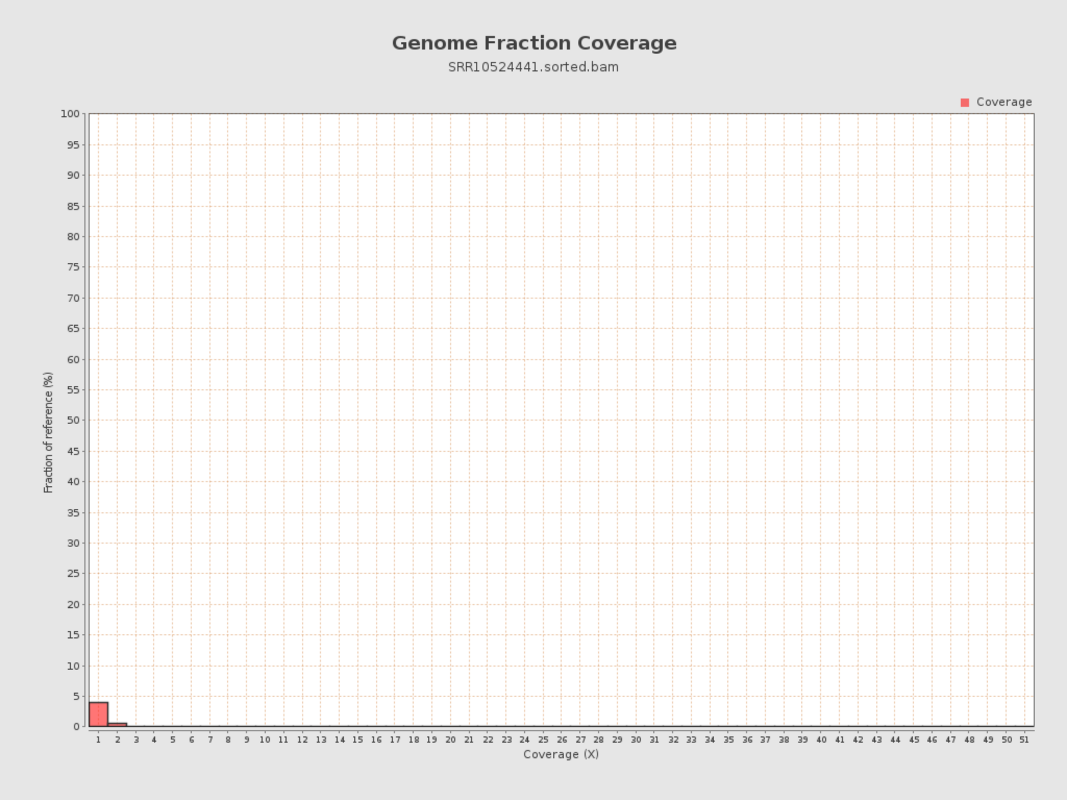
4. Results : Coverage Histogram



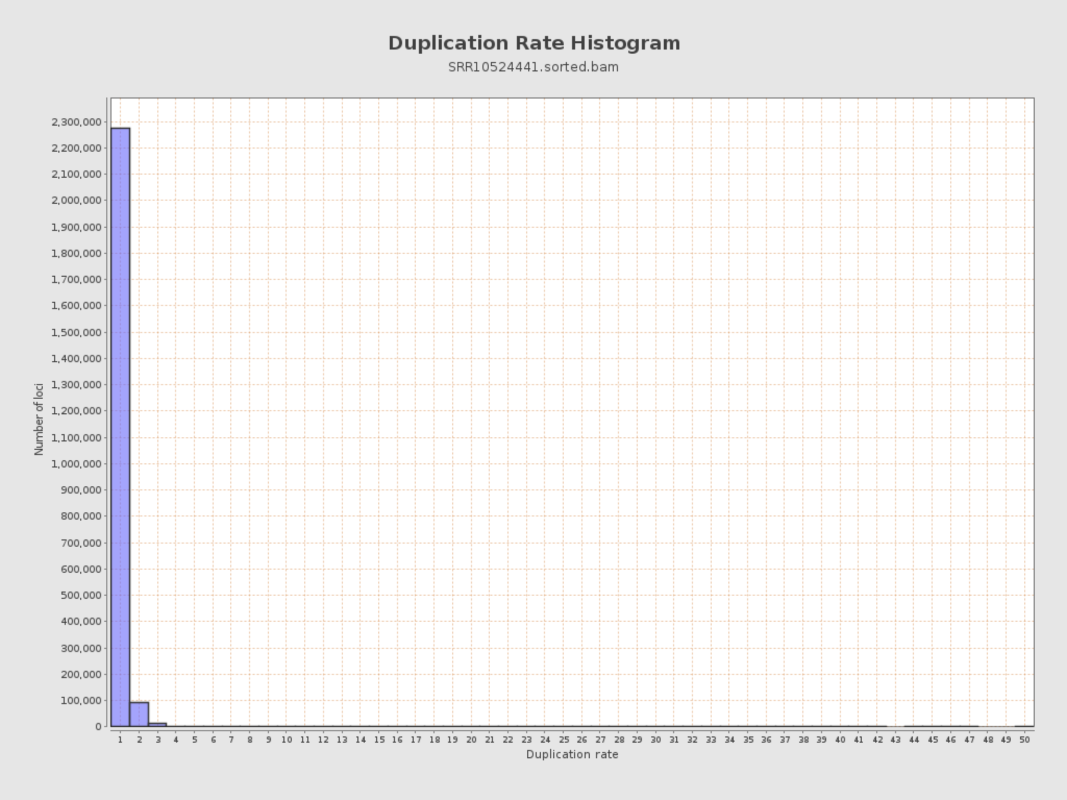
5. Results : Coverage Histogram (0-50X)



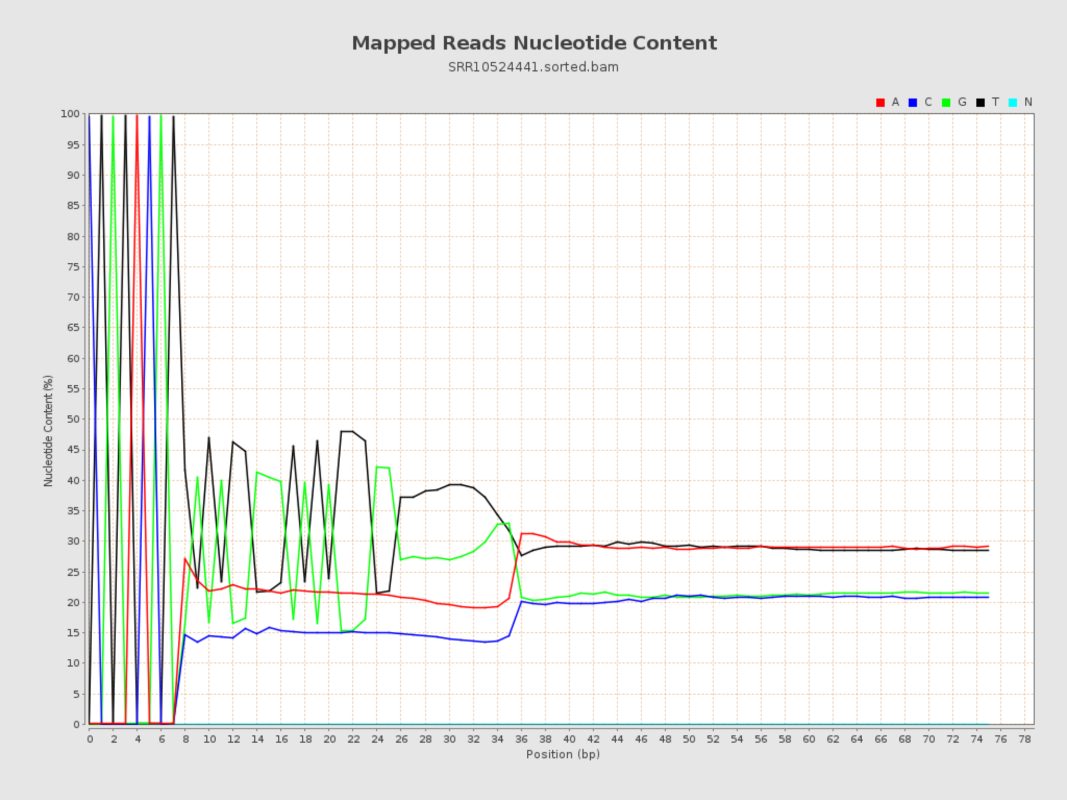
6. Results : Genome Fraction Coverage



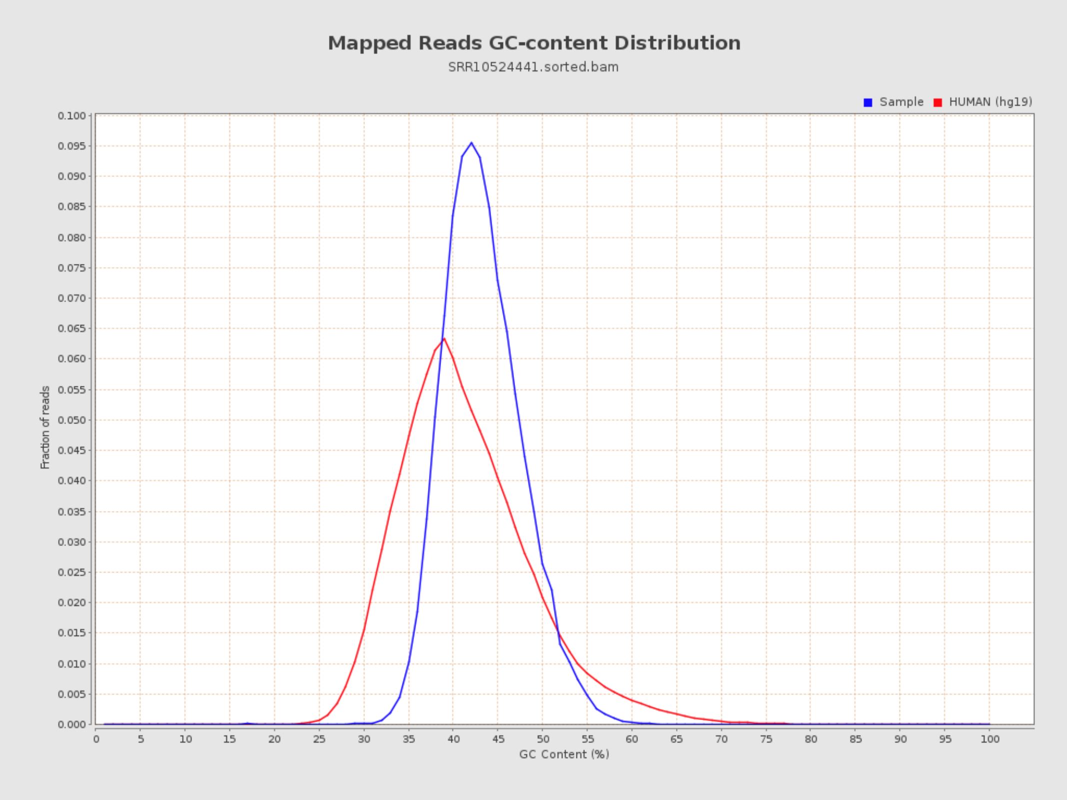
7. Results : Duplication Rate Histogram



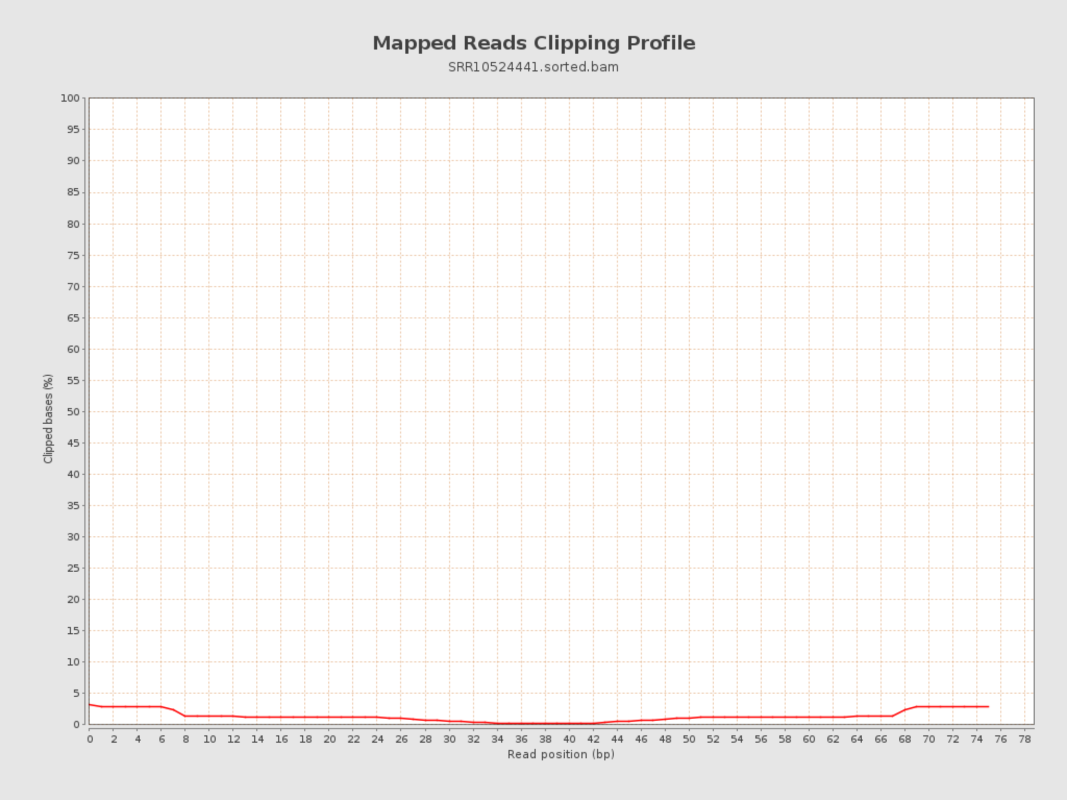
8. Results : Mapped Reads Nucleotide Content



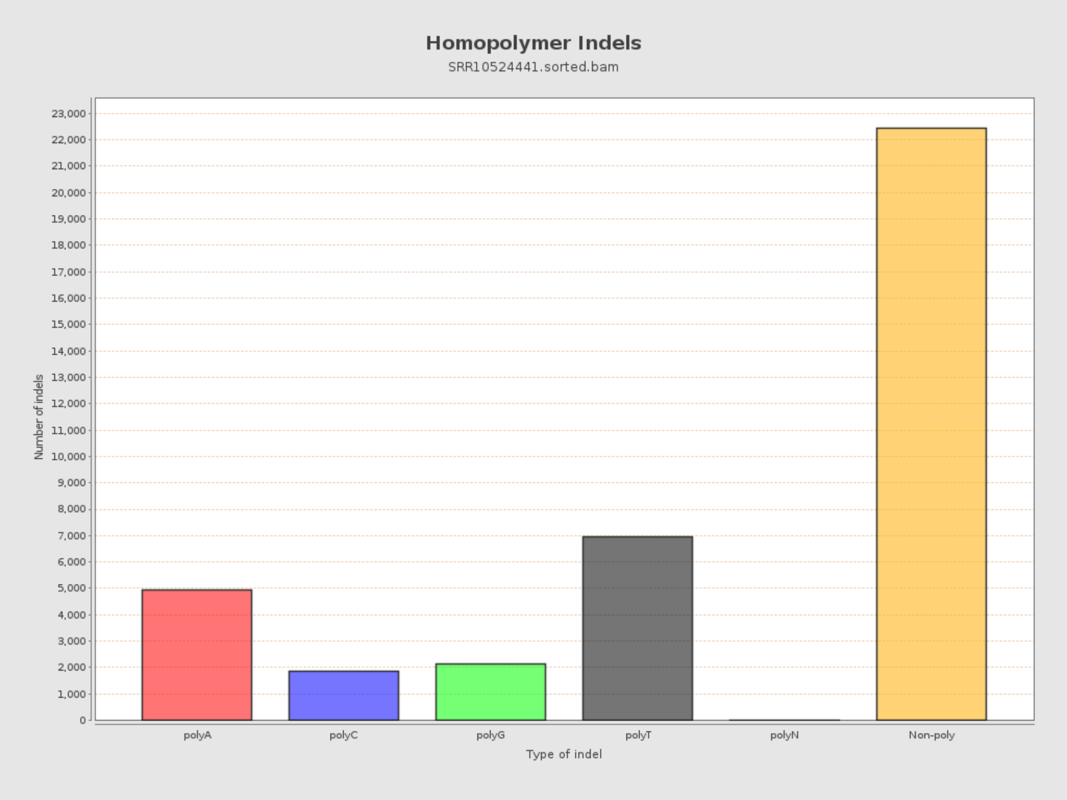
9. Results : Mapped Reads GC-content Distribution



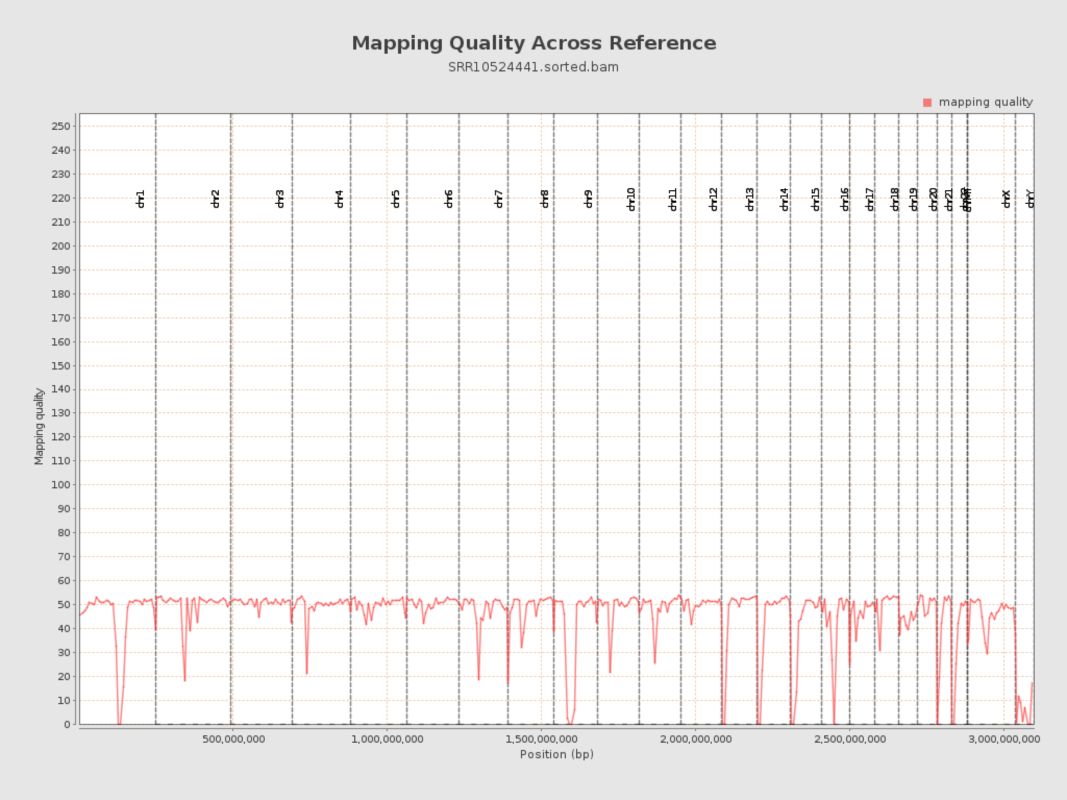
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram